



SEQUENCE LISTING

TECH CENTER 1600/2900

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RECEIVED

<110> King, Kendall W  
Madura, Rebecca A  
Rosey, Everett L

<120> NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA PNEUMONIAE  
mhp3 GENE AND USES THEREOF

<130> PC10555A

<140> PC10555

<141> 1999-09-29

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 1692

<212> DNA

<213> Mycoplasma hyopneumoniae

<300>

<400> 1

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<210> 2

<211> 451

<212> PRT

<213> Mycoplasma hyopneumoniae

<400> 2

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Glu	Thr	Thr	Lys	Glu	Glu	Lys	Ser	Ala	Asp	Asn	Gln	Asn	Lys	Gln	Ile
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Thr	Asp	Val	Ser	Lys	Ile	Ser	Gly	Leu	Val	Asn	Glu	Arg	Lys	Ser	Glu
	50					55					60				
Ile	Met	Ala	Ala	Lys	Ala	Asp	Ala	Asn	Lys	His	Phe	Gly	Leu	Asn	Met
65					70					75					80
Ala	Ile	Val	Thr	Ala	Gly	Gly	Thr	Val	Asn	Asp	Asn	Ser	Phe	Asn	Gln
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Ser	Ser	Trp	Glu	Ala	Ile	Gln	Gln	Leu	Gly	Ala	Leu	Thr	Gly	Gly	Glu
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Ile	Thr	Ser	Val	Asp	Ser	Ser	Thr	Ala	Glu	Leu	Glu	Gly	Lys	Tyr	Ser
			115				120						125		
Ser	Leu	Ala	Asn	Thr	Asn	Lys	Asn	Val	Trp	Val	Leu	Ser	Gly	Phe	Gln
			130				135						140		
His	Gly	Asp	Ala	Phe	Thr	Arg	Trp	Leu	Lys	Ile	Pro	Glu	Asn	Lys	Gln
145					150					155					160
Leu	Phe	Thr	Glu	Lys	Asn	Ile	Ile	Ile	Leu	Gly	Ile	Asp	Trp	Thr	Asp
				165					170						175

Thr	Glu	Asn	Val	Ile	Pro	Thr	Gly	Arg	Tyr	Ile	Asn	Leu	Thr	Tyr	Lys	180	185	190
Thr	Glu	Glu	Ala	Gly	Trp	Leu	Ala	Gly	Tyr	Ala	Asn	Ala	Ser	Phe	Leu	195	200	205
Ala	Lys	Lys	Phe	Pro	Ser	Asp	Pro	Thr	Lys	Arg	Ser	Ala	Ile	Val	Ile	210	215	220
Gly	Gly	Gly	Ile	Ser	Pro	Ala	Val	Thr	Asp	Phe	Ile	Ala	Gly	Tyr	Leu	225	230	235 240
Ala	Gly	Ile	Lys	Ala	Trp	Asn	Leu	Lys	Asn	Ser	Asp	Lys	Lys	Thr	Lys	245	250	255
Ile	Thr	Thr	Asp	Lys	Ile	Glu	Ile	Asn	Leu	Gly	Phe	Asp	Val	Gln	Asp	260	265	270
Thr	Ser	Thr	Lys	Glu	Arg	Leu	Glu	Gln	Ile	Ala	Ser	Lys	Asp	Lys	Pro	275	280	285
Ser	Thr	Leu	Leu	Ala	Val	Ala	Gly	Pro	Leu	Thr	Glu	Ile	Phe	Ser	Asp	290	295	300
Ile	Ile	Ala	Asn	Gln	Asn	Asp	Arg	Tyr	Leu	Ile	Gly	Val	Asp	Thr	Asp	305	310	315 320
Gln	Ser	Leu	Val	Tyr	Thr	Lys	Thr	Lys	Asn	Lys	Phe	Phe	Thr	Ser	Ile	325	330	335
Leu	Lys	Asn	Leu	Gly	Tyr	Ser	Val	Phe	Ser	Val	Leu	Ser	Asp	Leu	Tyr	340	345	350
Thr	Lys	Lys	Ser	Asn	Ser	Arg	Asn	Leu	Ala	Gly	Phe	Glu	Phe	Gly	Lys	355	360	365
Lys	Ser	Ala	Thr	Val	Tyr	Leu	Gly	Ile	Lys	Asp	Arg	Phe	Val	Asp	Ile	370	375	380
Ala	Asp	Thr	Ser	Leu	Glu	Gly	Asn	Asp	Lys	Lys	Leu	Ala	Thr	Glu	Ala	385	390	395 400
Ile	Ser	Glu	Ala	Lys	Lys	Glu	Phe	Glu	Glu	Lys	Thr	Lys	Thr	Ile	Pro	405	410	415
Ala	Glu	Glu	Val	Arg	Lys	Thr	Leu	Glu	Ile	Pro	Glu	Met	Pro	Asp	Lys	420	425	430

Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu Ile Thr Asp Ile  
 435 440 445

Asn Lys Asn  
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<210> 3  
 <211> 1263  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mhp3  
 manipulated for in vitro expression

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 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 180  
 gtaaagtata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240  
 actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300  
 tcacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cggatgatgc 360  
 ttcacaagat ggtaaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 420  
 atactcggaa ttgactggac tgatactgaa aatgtaattc caacagggtc atatatat 480  
 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg 540  
 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 600  
 tcgccagctg taactgattt tatcgctggt tatctagccg gaattaaagc ttggaatcta 660  
 aaaaattctg ataaaaaac aaagataaca actgataaaa tcgagataaa tcttgggttt 720  
 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780  
 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcgatat aatcgcaaac 840  
 caaaatgatc gttatctcat tgggtgttgac accgaccaat cacttgttta taaaaaac 900  
 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960  
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 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1140  
 gaagaaaaaa ctaagacaat tctgcccga gaagttcgta aaactttaga aattccggaa 1200  
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<210> 4  
 <211> 423  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mhp3

manipulated for in vitro expression

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		20						25					30		
Arg	Lys	Ser	Glu	Ile	Met	Ala	Ala	Lys	Ala	Asp	Ala	Asn	Lys	His	Phe
		35					40						45		
Gly	Leu	Asn	Met	Ala	Ile	Val	Thr	Ala	Gly	Gly	Thr	Val	Asn	Asp	Asn
	50					55					60				
Ser	Phe	Asn	Gln	Ser	Gly	Trp	Glu	Ala	Ile	Gln	Gln	Leu	Gly	Ala	Leu
65					70					75					80
Thr	Gly	Gly	Glu	Ile	Thr	Ser	Val	Asp	Ser	Ser	Thr	Ala	Glu	Leu	Glu
				85					90					95	
Gly	Lys	Tyr	Ser	Ser	Leu	Ala	Asn	Thr	Asn	Lys	Asn	Val	Trp	Val	Leu
			100					105					110		
Ser	Gly	Phe	Gln	His	Gly	Asp	Ala	Phe	Thr	Arg	Trp	Leu	Lys	Ile	Pro
		115					120					125			
Glu	Asn	Lys	Gln	Leu	Phe	Thr	Glu	Lys	Asn	Ile	Ile	Ile	Leu	Gly	Ile
	130						135					140			
Asp	Trp	Thr	Asp	Thr	Glu	Asn	Val	Ile	Pro	Thr	Gly	Arg	Tyr	Ile	Asn
145					150					155				160	
Leu	Thr	Tyr	Lys	Thr	Glu	Glu	Ala	Gly	Trp	Leu	Ala	Gly	Tyr	Ala	Asn
			165						170					175	
Ala	Ser	Phe	Leu	Ala	Lys	Lys	Phe	Pro	Ser	Asp	Pro	Thr	Lys	Arg	Ser
			180					185					190		
Ala	Ile	Val	Ile	Gly	Gly	Gly	Ile	Ser	Pro	Ala	Val	Thr	Asp	Phe	Ile
		195					200					205			
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	210					215					220				
Lys	Lys	Thr	Lys	Ile	Thr	Thr	Asp	Lys	Ile	Glu	Ile	Asn	Leu	Gly	Phe
225					230					235				240	

Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser  
245 250 255

Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu  
260 265 270

Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly  
275 280 285

Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe  
290 295 300

Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu  
305 310 315 320

Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe  
325 330 335

Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg  
340 345 350

Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu  
355 360 365

Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr  
370 375 380

Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu  
385 390 395 400

Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu  
405 410 415

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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<210> 5

<211> 602

<212> DNA

<213> Mycoplasma hyopneumoniae

<400> 5

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accgttccac cagcgggttac aattgccata tttagcccaa aatgtttgtt tgcacagct 300

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 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccaaagaaat 480  
 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattggtt taattacgat 540  
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<210> 6

<211> 200

<212> PRT

<213> Mycoplasma hyopneumoniae

<400> 6

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Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser  
 35 40 45

Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro  
 50 55 60

Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe  
 65 70 75 80

Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu  
 85 90 95

Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr  
 100 105 110

Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser  
 115 120 125

Ala Asp Phe Ser Ser Leu Val Val Ser Leu Ser Gln His Pro Ala Glu  
 130 135 140

Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn  
 145 150 155 160

Leu Phe His Phe Ile Phe Phe Phe Ile Val Val Leu Leu Ile Asn Cys  
 165 170 175

Phe Asn Tyr Asp Asp Phe Gln Leu Phe Phe Asn Lys Leu Ile Phe Ile

180

185

190

Leu His Phe Leu Leu Tyr Ser Lys  
 195 200

&lt;210&gt; 7

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Mycoplasma hyopneumoniae

&lt;400&gt; 7

Ala Gly Xaa Trp Ala Lys Glu Thr Thr Lys Glu Glu Lys Ser  
 1 5 10

&lt;210&gt; 8

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:  
 Oligonucleotide

&lt;400&gt; 8

Ala Trp Val Thr Ala Asp Gly Thr Val Asn  
 1 5 10

&lt;210&gt; 9

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:  
 Oligonucleotide

&lt;400&gt; 9

Ala Ile Val Thr Ala Asp Gly Thr Val Asn Asp Asn Lys Pro Asn Gln  
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Trp Val Arg Lys Tyr  
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&lt;210&gt; 10



<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 10  
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<210> 11  
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<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 11  
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<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 12  
tgrgtnacng cngayggnac ngtnaay

27

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 13

tgagtwacwg cwgatggwac wgtwaat

27

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 14

rttnacngtn ccrtcngcng tnacyc

26

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 15

attsacsgts ccatcsgcsg tsactc

26

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 16

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21

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 17

gaacgaaaat ccgaaattat gg

22

<210> 18

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 18

ctatctactg aagaatctca cc

22

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 19

gtgatgccgt tcacaagatg

20

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 20

cactaagaac gctgaaaacg g

21

<210> 21

<211> 21

<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 21  
gattacaact gtaaaatcga g 21

<210> 22  
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<212> DNA  
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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 22  
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<210> 23  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 23  
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<210> 24  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 24  
gaaatgcctg ataaacaacc 20

<210> 25  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 25  
cttcagaaat ggcttcagtt gc 22

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 26  
gctagataac cagcgataaa atcag 25

<210> 27  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 27  
tgcataatcc tgatttatc 19

<210> 28  
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<223> Description of Artificial Sequence:

Oligonucleotide

<400> 28

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22

<210> 29

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

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aatcggcata tgtgggataa agaaacaact aaag

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<210> 30

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

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<210> 31

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 31

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23

<210> 32

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 32

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28

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 33

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28

<210> 34

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 34

gataaaatgg aataaatttc ttgg

24

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 35

cagggtggga ggcaattcaa c

21

<210> 36

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide

<400> 36

caaaaatggt tgggtacttt ctgg

24

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide

<400> 37

cacaagatgg ttaaaaatcc c

21

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide

<400> 38

ggaattgact ggactgatac tg

22

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide



<400> 39  
gccggatggc ttgcaggata tg

22

<210> 40  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 40  
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24

<210> 41  
<211> 457  
<212> PRT  
<213> Mycoplasma hyorhinitis

<400> 41  
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20 25 30  
Gly Lys Ile Ile Arg Ile Phe Asp Asn Ser Phe Val Lys Asp Arg Gln  
35 40 45  
Ala Glu Ile Glu Lys Ala Lys Asn Phe Asp Phe Asn Thr Val Leu Leu  
50 55 60  
Thr Ala Gly Gly Thr Val Gln Asp Lys Ser Phe Asn Gln Ser Ile Trp  
65 70 75 80  
Glu Ala Val Leu Glu His Tyr Asp Gln Ile Glu Lys Thr Thr Asn Leu  
85 90 95  
Asp Arg Val Ser Gln Glu Thr Asn Asn Gln Ser Glu Leu Ile Gly Lys  
100 105 110  
Tyr Lys Asn Phe Leu Asn Gly Asn Lys Asn Val Trp Ile Leu Thr Gly  
115 120 125

Phe Gln Gln Gly Gln Glu Phe Pro Lys Phe Leu Lys Gln Thr Asp Ser  
 130 135 140

Asn Gly Lys Lys Tyr Ser Asp Leu Leu Ala Glu Lys Lys Val Ile Ile  
 145 150 155 160

Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys  
 165 170 175

Ala Gly His Phe Ile Ser Leu Leu Tyr Lys Thr Glu Glu Ala Gly Phe  
 180 185 190

Ile Ala Gly Tyr Ala Ser Ser Lys Phe Leu Ala Tyr Lys Phe Pro Asn  
 195 200 205

Asp Glu Ala Lys Arg Thr Ile Ala Pro Phe Gly Gly Gly His Gly Ala  
 210 215 220

Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr  
 225 230 235 240

Asn Asn Asp Asn Pro Thr Ala Lys Val Thr Ile Ser Asp Asn Asn Ile  
 245 250 255

Asn Ile Asp Thr Gly Phe Ile Ser Asn Asp Lys Thr Ala Thr Phe Ile  
 260 265 270

Asn Gly Ile Val Asn Lys Ser Ser Leu Val Leu Pro Val Ala Gly Ser  
 275 280 285

Leu Thr Ser Ser Val Val Asp Ala Ile Lys Lys Ser Asn Lys Asp Thr  
 290 295 300

Lys Tyr Leu Ile Gly Val Asp Thr Asp Gln Ser Lys Ile Phe Ser Pro  
 305 310 315 320

Ala Thr Val Phe Phe Thr Ser Ile Glu Lys His Leu Gly Arg Thr Ile  
 325 330 335

Tyr Gln Val Leu Thr Asp Ile Trp Leu Lys Lys Glu Asp Ser Lys Phe  
 340 345 350

Leu Gly Ser Phe Arg Ser Phe Lys Leu Thr Asn Pro Ala Asn Ala Thr  
 355 360 365

Val Tyr Lys Gly Ile Ser Asp Asp Phe Val Gly Val Ser Asn Ser Thr  
 370 375 380

Val Ala Asp Ala Asp Lys Val Lys Ala Gln Glu Phe Leu Asn Glu Ala  
385 390 395 400

Thr Ala Asp Phe Lys Lys Gln Ile Gln Ala Asn Pro Thr Asn Tyr Lys  
405 410 415

Ser Val Leu Gly Ile Pro Thr Met Leu Ile Asn Asp Asn Asp Ala Lys  
420 425 430

Asp Asn Glu Lys Ala Ser Leu Phe His Phe Asp Asn Trp Gln Thr Tyr  
435 440 445

Trp Ala Phe His Ser Arg Phe Ile Asn  
450 455

<210> 42

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial  
Sequence

<400> 42

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1

#6  
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21601

SEQUENCE LISTING

<110> King, Kendall W  
Madura, Rebecca A  
Rosey, Everett L

<120> NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA PNEUMONIAE  
mhp3 GENE AND USES THEREOF

<130> PC10555

<140>

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<150> US 60/156,602

<151> 1999-09-29

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1692

<212> DNA

<213> Mycoplasma hyopneumoniae

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gtttttgaat ataatagaaa atgtaaaata aaaattaatt tattaataaaa taattgaaag 60  
tcatcgtaat taaaacaatt aattaggaga acaactatga aaaaaaagat aaaatgaaat 120  
aaatttcttg gcttaggctt agtttttccg ctttcagcaa tcgcgacaat ctctgccgga 180  
tggtgggata aagaaacaac taaagaagaa aaatcagccg ataatacaaaa taagcaaatc 240  
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aaagctgatg caaacaaaac ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 360  
gtaaatgata attcatttaa ccaatcaagt tgagaggcaa ttcaacaact tggcgctctt 420  
actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 480  
tcaacttgcta ataccaacaa aaatgtttga gtactttctg gttttcaaca cgggtgatgcg 540  
ttcacaagat gattaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 600  
ataactcgaa ttgactgaac tgatactgaa aatgtaattc caacaggctc atataattaat 660  
ttaacctata aaactgaaga agccggatga cttgcaggat atgcgaatgc ttcctttttg 720  
gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 780  
tcgccagctg taactgattt tatcgctggt tatctagccg gaattaaagc ttgaaatcta 840  
aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggggtt 900  
gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 960  
tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 1020  
caaaatgata gttatctcat tgggtgttgac accgaccaat cacttgttta tacaaaaact 1080  
aaaaataaat ttttcacctc aattttgaaa aatttaggtt actcgtttt cagcgttctt 1140  
agtgatttat ataccaaaaa atcaaattca agaaatttag ccggccttga atttggtaaa 1200  
aaaagtgcaa ccgttttatct tgggaattaaa gacaggtttg tcgatattgc tgatacttct 1260  
ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1320  
gaagaaaaaa ctaagacaat tcctgccgaa gaagtctgta aaactttaga aattccggaa 1380  
atgcctgata aacaacctga taagcaacag gaaagcttag acaactaat taccgatatt 1440  
aataaaaatt aagtaagaaa aaataacaat tttttaacat tatatctttt tttagagatt 1500  
aattttcttc taatttagtt taatttaata taaaattata ttaaattaaa aaaataaaaa 1560  
atccggacta tttttgttcc ggatttttta tttttgtgtt actatttaat ataagtata 1620  
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<210> 2

<211> 451



<212> PRT

<213> Mycoplasma hyopneumoniae

<400> 2

Met Lys Lys Lys Ile Lys Trp Asn Lys Phe Leu Gly Leu Gly Leu Val  
1 5 10 15  
Phe Pro Leu Ser Ala Ile Ala Thr Ile Ser Ala Gly Cys Trp Asp Lys  
20 25 30  
Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile  
35 40 45  
Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu  
50 55 60  
Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met  
65 70 75 80  
Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln  
85 90 95  
Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu  
100 105 110  
Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu Gly Lys Tyr Ser  
115 120 125  
Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln  
130 135 140  
His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln  
145 150 155 160  
Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp  
165 170 175  
Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys  
180 185 190  
Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu  
195 200 205  
Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile  
210 215 220  
Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu  
225 230 235 240  
Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys  
245 250 255  
Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp  
260 265 270  
Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro  
275 280 285  
Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp  
290 295 300

Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp  
 305 310 315 320  
 Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile  
 325 330 335  
 Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr  
 340 345 350  
 Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys  
 355 360 365  
 Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile  
 370 375 380  
 Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala  
 385 390 395 400  
 Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro  
 405 410 415  
 Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys  
 420 425 430  
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 435 440 445  
 Asn Lys Asn  
 450

<210> 3  
 <211> 1269  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mhp3  
 manipulated for in vitro expression

<400> 3  
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 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 120  
 aaagctgatg caaacaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 180  
 gtaaatagata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240  
 actggagggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300  
 tcacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cggatgatgcg 360  
 ttcacaagat ggtaaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 420  
 atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggtcg atatatataat 480  
 ttaacctata aaactgaaga agcgggatgg cttgcaggat atgcgaatgc ttcctttttg 540  
 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 600  
 tcgccagctg taactgattt tatcgtgtgt tatctagccg gaattaaagc ttggaatcta 660  
 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttggggtt 720  
 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780  
 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 840  
 caaaatgatc gttatctcat tgggtgtgac accgaccaat cacttggtta taaaaaaact 900  
 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960  
 agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa 1020  
 aaaagtgcac ccgtttatct tgggaattaaa gacaggtttg tcgatattgc tgatacttct 1080

ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1140  
 gaagaaaaaa ctaagacaat tcctgccgaa gaagttcgta aaactttaga aattccggaa 1200  
 atgcctgata aacaacctga taagcaacag gaaagcttag acaaactaat taccgatatt 1260  
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<210> 4  
 <211> 423  
 <212> PRT  
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<220>  
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<400> 4  
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 1 5 10 15  
 Asn Lys Gln Ile Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu  
 20 25 30  
 Arg Lys Ser Glu Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe  
 35 40 45  
 Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn  
 50 55 60  
 Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu  
 65 70 75 80  
 Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu  
 85 90 95  
 Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu  
 100 105 110  
 Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro  
 115 120 125  
 Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile  
 130 135 140  
 Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn  
 145 150 155 160  
 Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn  
 165 170 175  
 Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser  
 180 185 190  
 Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile  
 195 200 205  
 Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp  
 210 215 220  
 Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe  
 225 230 235 240

Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser  
                     245                    250                    255  
 Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu  
                     260                    265                    270  
 Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly  
                     275                    280                    285  
 Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe  
                     290                    295                    300  
 Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu  
 305                    310                    315                    320  
 Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe  
                     325                    330                    335  
 Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg  
                     340                    345                    350  
 Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu  
                     355                    360                    365  
 Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr  
                     370                    375                    380  
 Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu  
 385                    390                    395                    400  
 Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu  
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 Ile Thr Asp Ile Asn Asn Leu  
                     420

<210> 5  
 <211> 602  
 <212> DNA  
 <213> Mycoplasma hyopneumoniae

<400> 5  
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 gagctatatt ttctttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca 180  
 gtaagagcgc caagttgttg aattgcctct caacttgatt ggtaaataga attatcattt 240  
 accgttccac cagcggttac aattgccata tttagcccaa aatgtttgtt tgcacagct 300  
 tttgcggcca taatttcgga ttttcgttca ttaactagtc ctgaaatttt tgagacatca 360  
 gtgatttgct tattttgatt atcggtgat ttttcttctt tagttgtttc tttatcccaa 420  
 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccaaagaaat 480  
 ttatttcatt ttatcttttt ttcatagtt gttctcctaa ttaattgttt taattacgat 540  
 gactttcaat tattttttta taaattaatt tttattttac attttctatt atattcaaaa 600  
 ac 602

<210> 6  
 <211> 200  
 <212> PRT



<213> Mycoplasma hyopneumoniae

<400> 6

Met Ile Ile Phe Phe Ser Val Asn Asn Cys Leu Phe Ser Gly Ile Phe  
1 5 10 15  
Asn His Leu Val Asn Ala Ser Pro Cys Trp Lys Pro Glu Ser Thr Gln  
20 25 30  
Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser  
35 40 45  
Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro  
50 55 60  
Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe  
65 70 75 80  
Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu  
85 90 95  
Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr  
100 105 110  
Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser  
115 120 125  
Ala Asp Phe Ser Ser Leu Val Val Ser Leu Ser Gln His Pro Ala Glu  
130 135 140  
Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn  
145 150 155 160  
Leu Phe His Phe Ile Phe Phe Phe Ile Val Val Leu Leu Ile Asn Cys  
165 170 175  
Phe Asn Tyr Asp Asp Phe Gln Leu Phe Phe Asn Lys Leu Ile Phe Ile  
180 185 190  
Leu His Phe Leu Leu Tyr Ser Lys  
195 200

<210> 7

<211> 14

<212> PRT

<213> Mycoplasma hyopneumoniae

<220>

<221> UNSURE

<222> 3

<223> Incomplete sequence obtained from publication WO 96/28472

<400> 7

Ala Gly Xaa Trp Ala Lys Glu Thr Thr Lys Glu Glu Lys Ser  
1 5 10

<210> 8

<211> 10

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 8  
Ala Trp Val Thr Ala Asp Gly Thr Val Asn  
1 5 10

<210> 9  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 9  
Ala Ile Val Thr Ala Asp Gly Thr Val Asn Asp Asn Lys Pro Asn Gln  
1 5 10 15

Trp Val Arg Lys Tyr  
20

<210> 10  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<221>  
<222>  
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Oligonucleotide

<400> 10  
tgytgrgcna argaracnac naargargar 30

<210> 11  
<211> 30  
<212> DNA  
<213> Artificial Sequence

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Oligonucleotide

<400> 11  
tggtgagcwa aagaaacwac waaagaagaa 30

<210> 12  
<211> 27  
<212> DNA

<213> Artificial Sequence

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<221>

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 12

tgrgtnacng cngayggnac ngtnaay

27

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

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Oligonucleotide

<400> 13

tgagtwacwg cwgatggwac wgtwaat

27

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 14

rttnacngtn ccrtcngcng tnacyc

26

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 15

attsacsqts ccatcsgcsg tsactc

26

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:

Oligonucleotide

<400> 16  
tttgagacat cagtgatttg c 21

<210> 17  
<211> 22  
<212> DNA  
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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 17  
gaacgaaaat ccgaaattat gg 22

<210> 18  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 18  
ctatctactg aagaatctca cc 22

<210> 19  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 19  
gtgatgccgt tcacaagatg 20

<210> 20  
<211> 21  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 20  
cactaagaac gctgaaaacg g 21

<210> 21  
<211> 21

<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 21  
gattacaact gtaaaatcga g 21

<210> 22  
<211> 20  
<212> DNA  
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Oligonucleotide

<400> 22  
ggctttcttca gttttatagg 20

<210> 23  
<211> 18  
<212> DNA  
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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 23  
aaactcgcaa ctgaagcc 18

<210> 24  
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<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 24  
gaaatgcctg ataaacaacc 20

<210> 25  
<211> 22  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 25

cttcagaaat ggcttcagtt gc

22

<210> 26  
<211> 25  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 26  
gctagataac cagcgataaa atcag

25

<210> 27  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 27  
tgcataatcc tgatttatc

19

<210> 28  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 28  
tgaaagtcac cgtaattaaa ac

22

<210> 29  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 29  
aatcggcata tgtgggataa agaaacaact aaag

34

<210> 30  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide  
  
 <400> 30  
 ggagtaatct agattattaa tatcggtaat taag 34  
  
 <210> 31  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide  
  
 <400> 31  
 gtttttgaat ataatagaaa atg 23  
  
 <210> 32  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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     Oligonucleotide  
  
 <400> 32  
 tttattaaaa aataattgaa agtcacgc 28  
  
 <210> 33  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide  
  
 <400> 33  
 ctattttgta attggcataa aaactgcc 28  
  
 <210> 34  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:  
     Oligonucleotide  
  
 <400> 34  
 gataaaatgg aataaatttc ttgg 24

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 35  
caggttggga ggcaattcaa c

21

<210> 36  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 36  
caaaaatggt tgggtacttt ctgg

24

<210> 37  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 37  
cacaagatgg ttaaaaatcc c

21

<210> 38  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide

<400> 38  
ggaattgact ggactgatac tg

22

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
Oligonucleotide



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Oligonucleotide

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<213> Mycoplasma hyorhinitis

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Gly Lys Ile Ile Arg Ile Phe Asp Asn Ser Phe Val Lys Asp Arg Gln  
35 40 45  
Ala Glu Ile Glu Lys Ala Lys Asn Phe Asp Phe Asn Thr Val Leu Leu  
50 55 60  
Thr Ala Gly Gly Thr Val Gln Asp Lys Ser Phe Asn Gln Ser Ile Trp  
65 70 75 80  
Glu Ala Val Leu Glu His Tyr Asp Gln Ile Glu Lys Thr Thr Asn Leu  
85 90 95  
Asp Arg Val Ser Gln Glu Thr Asn Asn Gln Ser Glu Leu Ile Gly Lys  
100 105 110  
Tyr Lys Asn Phe Leu Asn Gly Asn Lys Asn Val Trp Ile Leu Thr Gly  
115 120 125  
Phe Gln Gln Gly Gln Glu Phe Pro Lys Phe Leu Lys Gln Thr Asp Ser  
130 135 140  
Asn Gly Lys Lys Tyr Ser Asp Leu Leu Ala Glu Lys Lys Val Ile Ile  
145 150 155 160  
Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys  
165 170 175  
Ala Gly His Phe Ile Ser Leu Leu Tyr Lys Thr Glu Glu Ala Gly Phe  
180 185 190

Ile Ala Gly Tyr Ala Ser Ser Lys Phe Leu Ala Tyr Lys Phe Pro Asn  
 195 200 205  
 Asp Glu Ala Lys Arg Thr Ile Ala Pro Phe Gly Gly Gly His Gly Ala  
 210 215 220  
 Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr  
 225 230 235 240  
 Asn Asn Asp Asn Pro Thr Ala Lys Val Thr Ile Ser Asp Asn Asn Ile  
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 260 265 270  
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 275 280 285  
 Leu Thr Ser Ser Val Val Asp Ala Ile Lys Lys Ser Asn Lys Asp Thr  
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 385 390 395 400  
 Thr Ala Asp Phe Lys Lys Gln Ile Gln Ala Asn Pro Thr Asn Tyr Lys  
 405 410 415  
 Ser Val Leu Gly Ile Pro Thr Met Leu Ile Asn Asp Asn Asp Ala Lys  
 420 425 430  
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<130> 3153.00162/PC10555  
<140> US 09/676,249  
<141> 2000-09-29  
<150> US Prov. 60/156,602  
<151> 1999-09-29  
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RECEIVED

MAY 08 2003

TECH CENTER 1600/2900

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tcacgtgaat taaaacaatt aattaggaga acaactatga aaaaaaagat aaaatgaaat 120  
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gcaaaaaaat toccaagtga tccaactaaa agatcagcaa ttgttatcgg tgggtgggatt 780  
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tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 1020  
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Glu Thr Thr Lys Glu Glu Lys Ser Ala Asp Asn Gln Asn Lys Gln Ile  
 35 40 45

Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu  
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Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met  
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Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp  
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Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu  
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Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile  
210 215 220

Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu  
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245 250 255

Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp  
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Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro  
275 280 285

Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp  
290 295 300

Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp  
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Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile  
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Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr  
 340 345 350

Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys  
 355 360 365

Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile  
 370 375 380

Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala  
 385 390 395 400

Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro  
 405 410 415

Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys  
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 aaagctgatg caaacaaca ttttgggcta aatatggcaa ttgtaaccgc tgggtggaacg 180  
 gtaaataata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240  
 actggaggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300  
 tcacttgcta ataccaaca aaatgtttgg gtactttctg gttttcaaca cggtgatgag 360

ttcacaagat gggtaaaaat ccoctgaaaat aagcaattat ttactgaaaa aaatattatc	420
atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggtcg atatattaat	480
ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg	540
gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tggtgggatt	600
tcgccagctg taactgattt tatcgctggg tatctagccg gaattaaagc ttggaatcta	660
aaaaattctg ataaaaaac aaagataaca actgataaaa tcgagataaa tcttgggttt	720
gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct	780
tcaacactat tagctgtcgc tggaccactt actgaaattt tctcgatat aatcgcaaac	840
caaatgatc gttatctcat tgggtgtgac accgaccaat cacttgttta tacaaaaact	900
aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt	960
agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa	1020
aaaagtgcac cgttttatct tggaattaaa gacaggtttg tcgatattgc tgatacttct	1080
ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt	1140
gaagaaaaaa ctaagacaat tcttgccgaa gaagttcgta aaactttaga aattccggaa	1200
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 <223> Xaa is any amino acid

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Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn  
50 55 60

Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu  
65 70 75 80

Thr Gly Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu  
85 90 95

Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu  
100 105 110

Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro  
115 120 125

Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile  
130 135 140

Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn  
145 150 155 160

Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn  
165 170 175

Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser  
180 185 190

Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile  
195 200 205

Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp  
210 215 220

Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe  
225 230 235 240

Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser  
245 250 255



Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu  
 260 265 270

Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly  
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Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe  
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Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu  
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Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe  
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Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg  
 340 345 350

Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu  
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Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr  
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Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu  
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 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca 180

gtaagagcgc caagttgttg aattgcctct caacttgatt ggtaaata ga attatcattt 240  
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 gtgatttgct tattttgatt atcggctgat ttttcttctt tagttgtttc tttatcccaa 420  
 catccggcag agattgtcgc gattgctgaa agcggaaaaa ctaagcctaa gccagaagaat 480  
 ttatttcatt ttatcttttt tttcatagtt gttctcctaa ttaattgttt taattacgat 540  
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 20 25 30

Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser  
 35 40 45

Ala Val Glu Leu Ser Thr Glu Val Ile Ser Pro Pro Val Arg Ala Pro  
 50 55 60

Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe  
 65 70 75 80

Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu  
 85 90 95

Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr  
 100 105 110

Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser  
 115 120 125

Ala Asp Phe Ser Ser Leu Val Val Ser Leu Ser Gln His Pro Ala Glu

130

135

140

Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn  
 145 150 155 160

Leu Phe His Phe Ile Phe Phe Phe Ile Val Val Leu Leu Ile Asn Cys  
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Phe Asn Tyr Asp Asp Phe Gln Leu Phe Phe Asn Lys Leu Ile Phe Ile  
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Leu His Phe Leu Leu Tyr Ser Lys  
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35 40 45

Ala Glu Ile Glu Lys Ala Lys Asn Phe Asp Phe Asn Thr Val Leu Leu  
50 55 60

Thr Ala Gly Gly Thr Val Gln Asp Lys Ser Phe Asn Gln Ser Ile Trp  
65 70 75 80

Glu Ala Val Leu Glu His Tyr Asp Gln Ile Glu Lys Thr Thr Asn Leu  
85 90 95

Asp Arg Val Ser Gln Glu Thr Asn Asn Gln Ser Glu Leu Ile Gly Lys  
100 105 110

Tyr Lys Asn Phe Leu Asn Gly Asn Lys Asn Val Trp Ile Leu Thr Gly  
115 120 125

Phe Gln Gln Gly Gln Glu Phe Pro Lys Phe Leu Lys Gln Thr Asp Ser  
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Asn Gly Lys Lys Tyr Ser Asp Leu Leu Ala Glu Lys Lys Val Ile Ile  
145 150 155 160

Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys  
165 170 175

Ala Gly His Phe Ile Ser Leu Leu Tyr Lys Thr Glu Glu Ala Gly Phe  
180 185 190

Ile Ala Gly Tyr Ala Ser Ser Lys Phe Leu Ala Tyr Lys Phe Pro Asn  
195 200 205

Asp Glu Ala Lys Arg Thr Ile Ala Pro Phe Gly Gly Gly His Gly Ala  
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Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr  
225 230 235 240

Asn Asn Asp Asn Pro Thr Ala Lys Val Thr Ile Ser Asp Asn Asn Ile  
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Asn Ile Asp Thr Gly Phe Ile Ser Asn Asp Lys Thr Ala Thr Phe Ile  
260 265 270

Asn Gly Ile Val Asn Lys Ser Ser Leu Val Leu Pro Val Ala Gly Ser  
275 280 285

Leu Thr Ser Ser Val Val Asp Ala Ile Lys Lys Ser Asn Lys Asp Thr  
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Lys Tyr Leu Ile Gly Val Asp Thr Asp Gln Ser Lys Ile Phe Ser Pro  
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Ala Thr Val Phe Phe Thr Ser Ile Glu Lys His Leu Gly Arg Thr Ile  
325 330 335

Tyr Gln Val Leu Thr Asp Ile Trp Leu Lys Lys Glu Asp Ser Lys Phe  
340 345 350

Leu Gly Ser Phe Arg Ser Phe Lys Leu Thr Asn Pro Ala Asn Ala Thr  
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Val Tyr Lys Gly Ile Ser Asp Asp Phe Val Gly Val Ser Asn Ser Thr  
370 375 380

Val Ala Asp Ala Asp Lys Val Lys Ala Gln Glu Phe Leu Asn Glu Ala  
385 390 395 400

Thr Ala Asp Phe Lys Lys Gln Ile Gln Ala Asn Pro Thr Asn Tyr Lys  
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Ser Val Leu Gly Ile Pro Thr Met Leu Ile Asn Asp Asn Asp Ala Lys

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